



PCT

RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,428

TIME: 15:27:19

Input Set : A:\229576.txt

Output Set: N:\CRF4\07082004\J500428.raw

2 <110> APPLICANT: Sumitomo Pharmaceuticals CO., LTD.

W--> 3 <120> TITLE OF INVENTION: Therapeutic Agent for Anorexia Nervosa or Life-Style Related

W--> 4 Diseases, and Method for Screening Same

W--> 5 <130> FILE REFERENCE: 09517

C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/500,428

C--> 6 <141> CURRENT FILING DATE: 2004-06-28

6 <150> PRIOR APPLICATION NUMBER: JP 2001-397523

7 <151> PRIOR FILING DATE: 2001-12-27

9 <160> NUMBER OF SEQ ID NOS: 29

10 <170> SOFTWARE: PatentIn version 3.1

12 <210> SEQ ID NO: 1

13 <211> LENGTH: 1038

14 <212> TYPE: RNA

15 <213> ORGANISM: Homo sapiens

W--> 16 <220> FEATURE:

17 <221> NAME/KEY: CDS

18 <222> LOCATION: (1)..(1035)

20 <400> SEQUENCE: 1

21	aug uac aag gac ugc auc gag ucc acu gga gac uau uuu cuu cuc ugu	48
22	Met Tyr Lys Asp Cys Ile Glu Ser Thr Gly Asp Tyr Phe Leu Leu Cys	
23	1 5 10 15	
24	gac gcc gag ggg cca ugg ggc auc auu cug gag ucc cug gcc aua cuu	96
25	Asp Ala Glu Gly Pro Trp Gly Ile Ile Leu Glu Ser Leu Ala Ile Leu	
26	20 25 30	
27	ggc auc gug guc aca auu cug cua cuc uua gca uuu cuc uuc cuc aug	144
28	Gly Ile Val Val Thr Ile Leu Leu Leu Leu Ala Phe Leu Phe Leu Met	
29	35 40 45	
30	cga aag auc caa gac ugc agc cag ugg aa u guc cuc ccc acc cag cuc	192
31	Arg Lys Ile Gln Asp Cys Ser Gln Trp Asn Val Leu Pro Thr Gln Leu	
32	50 55 60	
33	cuc uuc cuc cug agu guc cug ggg cuc uuc gga cuc gcu uuu gcc uuc	240
34	Leu Phe Leu Leu Ser Val Leu Gly Leu Phe Gly Leu Ala Phe Ala Phe	
35	65 70 75 80	
36	auc auc gag cuc aa u caa caa acu gcc ccc gua cgc uac uuu cuc uuu	288
37	Ile Ile Glu Leu Asn Gln Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe	
38	85 90 95	
39	ggg guu cuc uuu gcu cuc ugu uuc uca ugc cuc uua gcu cau gcc ucc	336
40	Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ala His Ala Ser	
41	100 105 110	
42	aa u cua gug aag cug guu cgg ggu ugu guc ucc uuc ucc ugg acg aca	384
43	Asn Leu Val Lys Leu Val Arg Gly Cys Val Ser Phe Ser Trp Thr Thr	
44	115 120 125	
45	auu cug ugc auu gcu auu ggu ugc agu cug uug caa auc auu auu gcc	432

ENTERED

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46 Ile Leu Cys Ile Ala Ile Gly Cys Ser Leu Leu Gln Ile Ile Ile Ala
47      130      135      140
48 acu gag uau gug acu cuc aug acc aga ggu aug aug uuu gug aau      480
49 Thr Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Met Met Phe Val Asn
50 145      150      155      160
51 aug aca ccc ugc cag cuc aa uug gug gac uuu guu gua cuc cug guc uau      528
52 Met Thr Pro Cys Gln Leu Asn Val Asp Phe Val Val Leu Leu Val Tyr
53      165      170      175
54 guc cuc uuc cug aug gcc cuc aca uuc uuc guc ucc aaa gcc acc uuc      576
55 Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe
56      180      185      190
57 ugu ggc ccg ugu gag aac ugg aag cag cau gga agg cuc auc uuu auc      624
58 Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ile
59      195      200      205
60 acu gug cuc uuc ucc auc auc auc ugg gug gug ugg auc ucc aug cuc      672
61 Thr Val Leu Phe Ser Ile Ile Ile Trp Val Val Trp Ile Ser Met Leu
62      210      215      220
63 cug aga ggc aac ccg cag uuc cag cga cag ccc cag ugg gac gac ccg      720
64 Leu Arg Gly Asn Pro Gln Phe Gln Arg Gln Pro Gln Trp Asp Asp Pro
65 225      230      235      240
66 guc guc ugc auu gcu cug guc acc aac gca ugg guu uuc cug cug cug      768
67 Val Val Cys Ile Ala Leu Val Thr Asn Ala Trp Val Phe Leu Leu Leu
68      245      250      255
69 uac auc guc ccu gag cuc ugc auu cuc uac aga ucg ugu aga cag gag      816
70 Tyr Ile Val Pro Glu Leu Cys Ile Leu Tyr Arg Ser Cys Arg Gln Glu
71      260      265      270
72 ugc ccu uua caa ggc aa ugc gcc ugc ccc guc aca gcc uac caa cac agc      864
73 Cys Pro Leu Gln Gly Asn Ala Cys Pro Val Thr Ala Tyr Gln His Ser
74      275      280      285
75 uuc caa gug gag aac cag gag cuc ucc aga gcc cga gac agu gau gga      912
76 Phe Gln Val Glu Asn Gln Glu Leu Ser Arg Ala Arg Asp Ser Asp Gly
77      290      295      300
78 gcu gag gag gau gua gca uua acu uca uau ggu acu ccc auu cag ccg      960
79 Ala Glu Glu Asp Val Ala Leu Thr Ser Tyr Gly Thr Pro Ile Gln Pro
80 305      310      315      320
81 cag acu guu gau ccc aca caa gag ugu uuc auc cca cag gcu aaa cua      1008
82 Gln Thr Val Asp Pro Thr Gln Glu Cys Phe Ile Pro Gln Ala Lys Leu
83      325      330      335
84 agc ccc cag caa gau gca gga gga gua uaa      1038
85 Ser Pro Gln Gln Asp Ala Gly Gly Val
86      340      345
89 <210> SEQ ID NO: 2
90 <211> LENGTH: 345
91 <212> TYPE: PRT
92 <213> ORGANISM: Homo sapiens
W--> 93 <400> SEQUENCE: 2
94 Met Tyr Lys Asp Cys Ile Glu Ser Thr Gly Asp Tyr Phe Leu Leu Cys
95 1      5      10      15
97 Asp Ala Glu Gly Pro Trp Gly Ile Ile Leu Glu Ser Leu Ala Ile Leu

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98          20          25          30
100 Gly Ile Val Val Thr Ile Leu Leu Leu Ala Phe Leu Phe Leu Met
101          35          40          45
103 Arg Lys Ile Gln Asp Cys Ser Gln Trp Asn Val Leu Pro Thr Gln Leu
104          50          55          60
106 Leu Phe Leu Leu Ser Val Leu Gly Leu Phe Gly Leu Ala Phe Ala Phe
107 65          70          75          80
109 Ile Ile Glu Leu Asn Gln Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe
110          85          90          95
112 Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ala His Ala Ser
113          100          105          110
115 Asn Leu Val Lys Leu Val Arg Gly Cys Val Ser Phe Ser Trp Thr Thr
116          115          120          125
118 Ile Leu Cys Ile Ala Ile Gly Cys Ser Leu Leu Gln Ile Ile Ile Ala
119          130          135          140
121 Thr Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Met Met Phe Val Asn
122 145          150          155          160
124 Met Thr Pro Cys Gln Leu Asn Val Asp Phe Val Val Leu Leu Val Tyr
125          165          170          175
127 Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe
128          180          185          190
130 Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ile
131          195          200          205
133 Thr Val Leu Phe Ser Ile Ile Ile Trp Val Val Trp Ile Ser Met Leu
134          210          215          220
136 Leu Arg Gly Asn Pro Gln Phe Gln Arg Gln Pro Gln Trp Asp Asp Pro
137 225          230          235          240
139 Val Val Cys Ile Ala Leu Val Thr Asn Ala Trp Val Phe Leu Leu Leu
140          245          250          255
142 Tyr Ile Val Pro Glu Leu Cys Ile Leu Tyr Arg Ser Cys Arg Gln Glu
143          260          265          270
145 Cys Pro Leu Gln Gly Asn Ala Cys Pro Val Thr Ala Tyr Gln His Ser
146          275          280          285
148 Phe Gln Val Glu Asn Gln Glu Leu Ser Arg Ala Arg Asp Ser Asp Gly
149          290          295          300
151 Ala Glu Glu Asp Val Ala Leu Thr Ser Tyr Gly Thr Pro Ile Gln Pro
152 305          310          315          320
154 Gln Thr Val Asp Pro Thr Gln Glu Cys Phe Ile Pro Gln Ala Lys Leu
155          325          330          335
157 Ser Pro Gln Gln Asp Ala Gly Gly Val
158          340          345

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161 <210> SEQ ID NO: 3

162 <211> LENGTH: 1324

163 <212> TYPE: RNA

164 <213> ORGANISM: Mus musculus

W--> 165 <220> FEATURE:

166 <221> NAME/KEY: CDS

167 <222> LOCATION: (148) .. (1047)

W--> 168 <400> SEQUENCE: 3

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Input Set : A:\229576.txt

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169 gaggagagau uaaagcaccu gaaguugucu ccuccuuacu cauuugcagc cacagcuucc 60
171 ccaccagcac agccucagag gcuuccggag uagacucgga ggaggagacc agacaucggu 120
173 ucucgugagg ucuaccuaua agucacc aug uau gag gac ugc gug aag ucc aca 174
174 Met Tyr Glu Asp Cys Val Lys Ser Thr
175 1 5
176 gaa gac uau uac cuc uuc ugu gac aac gag ggg cca ugg gcc auu guu 222
177 Glu Asp Tyr Tyr Leu Phe Cys Asp Asn Glu Gly Pro Trp Ala Ile Val
178 10 15 20 25
179 cug gag ucc uug gca gug auu ggc aua gug guu acc aua uug cua cuc 270
180 Leu Glu Ser Leu Ala Val Ile Gly Ile Val Val Thr Ile Leu Leu Leu
181 30 35 40
182 cug gca uuu cug uuc cuc aug cgg aag guu cag gac ugc agc cag ugg 318
183 Leu Ala Phe Leu Phe Leu Met Arg Lys Val Gln Asp Cys Ser Gln Trp
184 45 50 55
185 aac gug cuu ccc acu cag uuc cuc uuc cug cug gcu gug cuc ggg cuc 366
186 Asn Val Leu Pro Thr Gln Phe Leu Phe Leu Leu Ala Val Leu Gly Leu
187 60 65 70
188 uuc gga cuu acu uuu gcc uuc auc auc caa cuc aac cau caa acu gcc 414
189 Phe Gly Leu Thr Phe Ala Phe Ile Ile Gln Leu Asn His Gln Thr Ala
190 75 80 85
191 ccu guu cgc uac uuc cuc uuu ggg guu cuc uuu gcu auc ugc uuc ucc 462
192 Pro Val Arg Tyr Phe Leu Phe Gly Val Leu Phe Ala Ile Cys Phe Ser
193 90 95 100 105
194 ugc cuc cug gcu cau gcc ucc aac cug gug aag cug guc cgg ggu aga 510
195 Cys Leu Leu Ala His Ala Ser Asn Leu Val Lys Leu Val Arg Gly Arg
196 110 115 120
197 guc ucc uuc ugc ugg aca aca auu cug uuc auu gcu auc ggu guc agc 558
198 Val Ser Phe Cys Trp Thr Thr Ile Leu Phe Ile Ala Ile Gly Val Ser
199 125 130 135
200 cug uug cag acc auc auu gcg aua gag uau gug acc cuc auc aug acc 606
201 Leu Leu Gln Thr Ile Ile Ala Ile Glu Tyr Val Thr Leu Ile Met Thr
202 140 145 150
203 aga ggc uug aug uuc gag cau aug aca ccg uau cag cuc aa u gug gac 654
204 Arg Gly Leu Met Phe Glu His Met Thr Pro Tyr Gln Leu Asn Val Asp
205 155 160 165
206 uuu guc ugu cuc cug auc uau guc cuc uuc cug aug gcc cuc acu uuc 702
207 Phe Val Cys Leu Leu Ile Tyr Val Leu Phe Leu Met Ala Leu Thr Phe
208 170 175 180 185
209 uuc guc ucc aag gcc acc uuc ugu ggc cca ugu gag aac ugg aaa cag 750
210 Phe Val Ser Lys Ala Thr Phe Cys Gly Pro Cys Glu Asn Trp Lys Gln
211 190 195 200
212 cac gga agg cuc aua uuu gcu acu gug cug guc ucu auc auu auc ugg 798
213 His Gly Arg Leu Ile Phe Ala Thr Val Leu Val Ser Ile Ile Ile Trp
214 205 210 215
216 gug gug ugg auc ucc aug cuc uug aga ggc aac ccc cag cuc cag cga 846
217 Val Val Trp Ile Ser Met Leu Leu Arg Gly Asn Pro Gln Leu Gln Arg
218 220 225 230
220 cag ccc cac ugg gac gau gca guc auc ugc auu ggc cug guc acc aac 894
221 Gln Pro His Trp Asp Asp Ala Val Ile Cys Ile Gly Leu Val Thr Asn

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222      235      240      245
224 gcu ugg guc uuc cug cug auc uac auc auc ccu gag cug agc aua cuc      942
225 Ala Trp Val Phe Leu Leu Ile Tyr Ile Ile Pro Glu Leu Ser Ile Leu
226 250      255      260      265
228 uac agg uca ugu agg cag gag ugu ccu aca caa ggc aac guc ugc cag      990
229 Tyr Arg Ser Cys Arg Gln Glu Cys Pro Thr Gln Gly Asn Val Cys Gln
230      270      275      280
232 guc ccu guc uac caa cgc agc uuc agg aug gau acc cag gaa ccc acc      1038
233 Val Pro Val Tyr Gln Arg Ser Phe Arg Met Asp Thr Gln Glu Pro Thr
234      285      290      295
235 aga gag ugc ugaucacagc cgggagauauc ucaucccauc agcuacacua      1087
236 Arg Glu Cys
237      300
238 agccacacagc aagaugcagg auuguaaagc uacuggaaac agcauagaga caaccuggaa      1147
240 gagugcccug cuccacacag ccuuaaagag cccaggggag cacuggacac acugucaaug      1207
242 aagcauccuu ccuguccuu ccucucuguu ucccugcccu uccacucuu cuggacccag      1267
244 ccucugaaga cugucauguc cugcacaauu aaaaucuuugu ugccacccua aaaaaaa      1324
247 <210> SEQ ID NO: 4
248 <211> LENGTH: 300
249 <212> TYPE: PRT
250 <213> ORGANISM: Mus musculus
W--> 251 <400> SEQUENCE: 4
252 Met Tyr Glu Asp Cys Val Lys Ser Thr Glu Asp Tyr Tyr Leu Phe Cys
253 1      5      10      15
255 Asp Asn Glu Gly Pro Trp Ala Ile Val Leu Glu Ser Leu Ala Val Ile
256      20      25      30
258 Gly Ile Val Val Thr Ile Leu Leu Leu Leu Ala Phe Leu Phe Leu Met
259      35      40      45
261 Arg Lys Val Gln Asp Cys Ser Gln Trp Asn Val Leu Pro Thr Gln Phe
262      50      55      60
264 Leu Phe Leu Leu Ala Val Leu Gly Leu Phe Gly Leu Thr Phe Ala Phe
265 65      70      75      80
267 Ile Ile Gln Leu Asn His Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe
268      85      90      95
270 Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Leu Ala His Ala Ser
271      100      105      110
273 Asn Leu Val Lys Leu Val Arg Gly Arg Val Ser Phe Cys Trp Thr Thr
274      115      120      125
276 Ile Leu Phe Ile Ala Ile Gly Val Ser Leu Leu Gln Thr Ile Ile Ala
277      130      135      140
279 Ile Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Leu Met Phe Glu His
280 145      150      155      160
282 Met Thr Pro Tyr Gln Leu Asn Val Asp Phe Val Cys Leu Leu Ile Tyr
283      165      170      175
285 Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe
286      180      185      190
288 Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ala
289      195      200      205
291 Thr Val Leu Val Ser Ile Ile Ile Trp Val Val Trp Ile Ser Met Leu

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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29

VERIFICATION SUMMARY

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Input Set : A:\229576.txt

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L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:283 W: Missing Blank Line separator, <220> field identifier
L:93 M:283 W: Missing Blank Line separator, <400> field identifier
L:165 M:283 W: Missing Blank Line separator, <220> field identifier
L:168 M:283 W: Missing Blank Line separator, <400> field identifier
L:251 M:283 W: Missing Blank Line separator, <400> field identifier
L:313 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:314 M:283 W: Missing Blank Line separator, <220> field identifier
L:318 M:283 W: Missing Blank Line separator, <400> field identifier
L:325 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:326 M:283 W: Missing Blank Line separator, <220> field identifier
L:330 M:283 W: Missing Blank Line separator, <400> field identifier
L:337 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:338 M:283 W: Missing Blank Line separator, <220> field identifier
L:342 M:283 W: Missing Blank Line separator, <400> field identifier
L:349 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:350 M:283 W: Missing Blank Line separator, <220> field identifier
L:355 M:283 W: Missing Blank Line separator, <400> field identifier
L:362 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:363 M:283 W: Missing Blank Line separator, <220> field identifier
L:367 M:283 W: Missing Blank Line separator, <400> field identifier
L:374 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:375 M:283 W: Missing Blank Line separator, <220> field identifier
L:379 M:283 W: Missing Blank Line separator, <400> field identifier
L:386 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:387 M:283 W: Missing Blank Line separator, <220> field identifier
L:391 M:283 W: Missing Blank Line separator, <400> field identifier
L:398 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:399 M:283 W: Missing Blank Line separator, <220> field identifier
L:403 M:283 W: Missing Blank Line separator, <400> field identifier
L:584 M:283 W: Missing Blank Line separator, <220> field identifier
L:588 M:283 W: Missing Blank Line separator, <400> field identifier
L:596 M:283 W: Missing Blank Line separator, <220> field identifier
L:600 M:283 W: Missing Blank Line separator, <400> field identifier
L:608 M:283 W: Missing Blank Line separator, <220> field identifier
L:612 M:283 W: Missing Blank Line separator, <400> field identifier
L:620 M:283 W: Missing Blank Line separator, <220> field identifier
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L:632 M:283 W: Missing Blank Line separator, <220> field identifier
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